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TO: EXAMINER MEDINA IBRAHIM; USPTO
FROM: GINNIE DRESS (virginia.dress@pioneer.com) *vm*
RE: US APPLICATION 10/782,436; Atty Docket 1121D
DATE: October 13, 2005 FAX NUMBER: (571) 273-0797
NUMBER OF PAGES FOLLOWING THIS SHEET: 21

Examiner Ibrahim,

Attached please find the requested information comprising a summary of percent sequence identity and the alignments, as determined by GAP analyses, for SEQ ID NOS: 2, 4, 6, 8, and 10 from the above referenced application.

Other GAP analyses are available, for example, vs. Arabidopsis RuvB (Rvb1).

Sincerely,
Virginia Dress
Reg. 48,243

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Application 10/782,436

Applicant Docket Ref: 1121D

1121D RuvB

GAP comparison of sequences in application as originally filed.

Polynucleotides – Percent Sequence Identity

SEQ ID	3	5	7	9
1	97.556	88.091	89.659	97.236
3	100	87.166	89.117	97.247
5	---	100	99.282	87.081
7	---	---	100	89.109

Polypeptides – Percent Sequence Identity

SEQ ID	4	6	8	10
2	99.341	96.923	96.923	99.543
4	100	97.582	97.582	100
6	---	100	100	97.489
8	---	---	100	97.489

Individual pairwise GAP alignments of polypeptides on following pages.

enablement - mod. to
align
from

10/782,436

1121D

571-273-
6797

claim 5

allowable

summary GAP
alignments

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RUVB
to: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RUVB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2253	Length:	455
Ratio:	4.952	Gaps:	0
Percent Similarity:	99.560	Percent Identity:	99.341

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID2 x 1121SID4 November 5, 2001 17:08 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQSAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQAAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

51 LAVDMIRQKKMAGRAVLLVGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 LAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEAEESTTCGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEAEESTTCGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

151 AKSISHVVIISLKT VKG TKQLKLDSS IYDALIKEKVAVGDVIYIEANS GAV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AKSISHVVIISLKT VKG TKQLKLDSS IYDALIKEKVAVGDVIYIEANS GAV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

201 KRVGRCD SFATEYDLEAE EYVPIPKGEVHK KKEIVQDVT LHDLD AANAQ P 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KRVGRCD SFATEYDLEAE EYVPIPKGEVHK KKEIVQDVT LHDLD AANAQ P 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

251 QGGQDILSLMGQMMKPRKTEITEKLRQSEINKV VNR YIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 QGGQDILSLMGQMMKPRKTEITEKLRQSEINKV VNR YIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

301 IDEVHMLDIECF SYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 IDEVHMLDIECF SYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Application 10/782,436

Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEDIDMDEESLAYLGEIGQQT 400
|||||
351 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEEIDMDEESLAYLGBIGQQT 400
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
|||||
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
451 ERYIT 455
|||||
451 ERYIT 455

Application 10/782.436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RuVB
to: 1121SID6 check: 8413 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 6 RuVB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2212	Length:	455
Ratio:	4.862	Gaps:	0
Percent Similarity:	97.363	Percent Identity:	96.923

```
Match display thresholds for the alignment(s):
      | = IDENTITY
      : = 2
      . = 1
```

1121SID2 x 1121SID6 November 5, 2001 17:09

```

1  MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQSAAREAAAG  50
  |||||||||||||||||||||||||||||..|||
1  MRIEEVQSTSKKQRIATHTHIKGLGLDANGMSMPLAAGFVGQAAAREAAAG  50

51  LAVDMIRQKKMAGRAVLLVGPPATGKTALALGIAQELGSKVPFCPMVGSE  100
  |||||..|||
51  LAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE  100

101  VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGEVTELSPEEAESTTGGY  150
  |||||||||||||||||||||||||||||
101  VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGEVIELSPPEEAESTTGGY  150

151  AKSISHVIIISLKTIVKGTKQLKLDSSIIDALIKEKVAVGDVIYIEANSGAV  200
  ||||||| ||||||| |||
151  AKSISHVIIIGLKTIVKGTKQLKLDPSIIDALIKEKVAVGDVIYIEANSGAV  200

201  KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP  250
  ||||||| ||||||| |||
201  KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP  250

251  QGGQDILSLMGQMMKPRKTEITEKLQEIKNVNVNRYIDEGIAELVPGVLF  300
  ||||||| ||||||| |||
251  QGGQDILSLMGQMMKPRKTEITEKLQEIKNVNVNRYIDEGIAELVPGVLF  300

301  IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGDTMTSPHGIP  350
  ||||||| ||||||| |||
301  IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGDTMTSPHGIP  350

```

Application 10/782,436

Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEDIDMDEESLAYLGEIGQQT 400
|||||:|||||
351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDEESLAYLGEIGQQT 400
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDAKSSARLLQEQQ 450
|||||:|||||
401 SLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDAKSSARLLQEQQ 450
451 ERYIT 455
|||||
451 ERYIT 455

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RuvB
to: 1121SID8 check: 2111 from: 1 to: 456
WPDEF Case 1121 SEQ ID NO: 8 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2202	Length:	456
Ratio:	4.840	Gaps:	1
Percent Similarity:	97.363	Percent Identity:	96.923

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

1121SID2 x 1121SID8

November 5, 2001 17:09 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLD.ANGMAIALAAGFVGQSAAREAA 49
|||||
1 MRIEEVQSTSKKQRIATHTHIKGLGLDQANGMSMPLAAGFVGQAAAREAA 50

50 GLAVDMIRQKKMAGRAVLLVGPPATGKTALALCIAQELGSKVPFCPMVGS 99
|||||
51 GLAVDMIRQKKMAGRALLLAGPPATGKTALALCIAQELGSKVPFCPMVGS 100

100 EVYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPEEAESTTGG 149
|||||
101 EVYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPEEAESTTGG 150

150 YAKSISHVVIISLKTVGKTKQLKLDSSIYDALYKEKVAVGDVYIEANSGA 199
|||||
151 YAKSISHVVIIGLKTVGKTKQLKLDPSIYDALIYKEKVAVGDVYIEANSGA 200

200 VKRVGRCDSPATEYDLEABEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 249
|||||
201 VKRVGRCDSPATEYDLEABEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250

250 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 299
|||||
251 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 300

300 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 349
|||||
301 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 350
```

Application 10/782,436

Applicant Docket Ref: 1121D

350 PVDLLDRLVIIRTETYGPTMIQILAIRAQVEDIDMDEESLAYLGEIGQQ 399
|||||
351 PVDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDEESLAYLGEIGQQ 400
|||||
400 TSLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQ 449
|||||
401 TSLRHAIQLLSPASVVAKTNGREKMKADLEEVSGLYLDKSSARLLQEQ 450
|||||
450 QERYIT 455
|||||
451 QERYIT 456

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RuvB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2129	Length:	455
Ratio:	4.861	Gaps:	2
Percent Similarity:	99.772	Percent Identity:	99.543

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

1121SID2 x 1121SID10 November 5, 2001 17:10 ..

```
1 MRIBEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQSAAREAAC 50
|||||
1 MRIBEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVG..... 41

51 LAVDMIRQKKMAGRAVLLVGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
|||||
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGSE 83

101 VYSSEVKKTEVLMENFRRATGLRIKENKEVYEGETELSPPEAESTTGGY 150
|||||
84 VYSSEVKKTEVLMENFRRATGLRIKENKEVYEGETELSPPEAESTTGGY 133

151 AKSISHVVIISLKTIVKGTQQLKLDSSIIYDALIKEKVAVGDVIYIEANSGAV 200
|||||
134 AKSISHVVIISLKTIVKGTQQLKLDSSIIYDALIKEKVAVGDVIYIEANSGAV 183

201 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250
|||||
184 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 233

251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 300
|||||
234 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 283

301 IDEVHMLDIECFSYLNRALESPLSPVILATNRGICNVRGTDMTSPHGIP 350
|||||
284 IDEVHMLDIECFSYLNRALESPLSPVILATNRGICNVRGTDMTSPHGIP 333
```

Application 10/782,436

Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEDIDMDEESLAYLGEIGQQT 400
|||||:|||||
334 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 383

401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
|||||
384 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 433

451 ERYIT 455
|||||
434 ERYIT 438

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RuvB
to: 1121SID6 check: 8413 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 6 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2222	Length:	455
Ratio:	4.884	Gaps:	0
Percent Similarity:	97.802	Percent Identity:	97.582

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID4 x 1121SID6 November 5, 2001 17:11 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMSMPLAAGFVGQAAAREAAAG 50

51 LAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 LAVDMIRQKKMAGRALLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100

101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEEAESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEEAESTTGGY 150

151 AKSISHVIIISLKTIVKGTQQLKLDSSIYDALIKEKVAVGCDVIYIEANS 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AKSISHVIIIGLKTIVKGTQQLKLDPSIYDALIKEKVAVGCDVIYIEANS 200

201 KRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250

251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 300

301 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
```

Application 10/782,436

Applicant Docket Ref: 1121D

```
351 VDLLDRLVIIRTETETGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 400
   |||||||||||||||||||||||||||||||||||||||
351 VDLLDRLVIIRTETETGPTMIQILAIRAQVEEIDIDEESLAYLGEIGQQT 400
   |||||||||||||||||||||||||||||||||||||||
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
   ||||||||:|||||.|||||.|||||||||||||||||
401 SLRHAIQLISPASVVAKTNGREKMCKADLEEVSGLYLDKSSARLLQEQQ 450
   |||||||
451 ERYIT 455
   |||||
451 ERYIT 455
```

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RuvB
to: 1121SID8 check: 2111 from: 1 to: 456
WPDEF Case 1121 SEQ ID NO: 8 RuvB
Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight: 8 Average Match: 2.912
Length Weight: 2 Average Mismatch: -2.003
Quality: 2212 Length: 456
Ratio: 4.862 Gaps: 1
Percent Similarity: 97.802 Percent Identity: 97.582

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

1121SID4 x 1121SID8

November 5, 2001 17:11 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLD.ANGMAIALAAGFVCQAAAREAA 49
|||||
1 MRIEEVQSTSKKQRIATHTHIKGLGLDQANGMSMPLAAGFVCQAAAREAA 50
50 GLAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGS 99
|||||
51 GLAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGS 100
100 EVYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEAESTTGG 149
|||||
101 EVYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETEVLSPPEAESTTGG 150
150 YAKSISHVVIISLKTVMGKTKQLKLDSSIYDALIKEKVAVGCVIYIEANSGA 199
|||||
151 YAKSISHVVIIGLKTVMGKTKQLKLDPSIYDALIKEKVAVGCVIYIEANSGA 200
200 VKRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 249
|||||
201 VKRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250
250 PQGGQDILSLMCQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 299
|||||
251 PQGGQDILSLMCQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 300
300 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 349
|||||
301 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 350
```

Application 10/782,436

Applicant Docket Ref: 1121D

350 PVDLLDRLVIRTETYGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQ 399
|||||
351 PVDLLDRLVIRTETYGPTMIQILAIRAQVEEIDIDEESLAYLGEIGQQ 400
|||||
400 TSLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQ 449
|||||
401 TSLRHAIQLLSPASVVAKTNGREKMKADLEEVSGLYLDKSSARLLQEQ 450
|||||
450 QERYIT 455
|||||
451 QERYIT 456

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RuvB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuvB
Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2136	Length:	455
Ratio:	4.877	Gaps:	2
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID4 x 1121SID10 November 5, 2001 17:11 ..

```
1 MRIEEVQSTSKKORIATHTHIKGLGLDANGMAIALAAGFVGQAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVG..... 41

51 LAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGCSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGCSE 83

101 VYSSEVKKTEVLMENFRRAIGLRIKENKEVYEGEVTELSPEEAESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
84 VYSSEVKKTEVLMENFRRAIGLRIKENKEVYEGEVTELSPEEAESTTGGY 133

151 AKSISHVVIISLKTIVKGTKQLKLDSSIIYDALIKEKVAVGDVIYIEANGAV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
134 AKSISHVVIISLKTIVKGTKQLKLDSSIIYDALIKEKVAVGDVIYIEANGAV 183

201 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
184 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 233

251 QGGQDILSLMGQMMKPRKTEITEKLRQEIINKVNNRYIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
234 QGGQDILSLMGQMMKPRKTEITEKLRQEIINKVNNRYIDEGIAELVPGVLF 283

301 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
284 IDEVHMLDIECFPSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 333
```

Application 10/782,436

Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 400
|||||
334 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 383
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
|||||
384 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 433
451 ERYIT 455
|||||
434 ERYIT 438

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Applicant Docket Ref: 1121D

GAP of: 1121SID6 check: 8413 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 6 RuvB
to: 1121SID8 check: 2111 from: 1 to: 456
WPDEF Case 1121 SEQ ID NO: 8 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2261	Length:	456
Ratio:	4.969	Gaps:	1
Percent Similarity:	100.000	Percent Identity:	100.000

```
Match display thresholds for the alignment(s):
      | = IDENTITY
      : = 2
      . = 1
```

1121SID6 x 1121SID8 November 5, 2001 17:12 ..

[illegible]

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Applicant Docket Ref: 1121D

350 PVDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDBESLAYLGEIGQQ 399
|||||
351 PVOLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDERSLAYLGEIGQQ 400
|||||
400 TSLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDKSSARLLQEQ 449
|||||
401 TSLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDKSSARLLQEQ 450
|||||
450 QERYIT 455
|||||
451 QERYIT 456

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID6 check: 8413 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 6 RuvB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight: 8 Average Match: 2.912
Length Weight: 2 Average Mismatch: -2.003
Quality: 2095 Length: 455
Ratio: 4.783 Gaps: 2
Percent Similarity: 97.717 Percent Identity: 97.489

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

1121SID6 x 1121SID10 November 5, 2001 17:13 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMSMPLAAGFVGQAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVG..... 41

51 LAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGSE 83

101 VYSSEVKKTEVLMENFRAICLRIKENKEVYEGEVIELSPPEEAESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
84 VYSSEVKKTEVLMENFRAICLRIKENKEVYEGEVTELSPEEAESTTGGY 133

151 AKSISHVIIIGLKTVMGKTKQLKLDPSIYDALIKEKVAVGDVIYIEANS 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
134 AKSISHVIIISLKTVMGKTKQLKLDSSIYDALIKEKVAVGDVIYIEANS 183

201 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
184 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 233

251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGV 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
234 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGV 283

301 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHG 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
284 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHG 333
```

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Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEEIDIDEESLAYLGEIGQQT 400
|||||
334 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 383
|||||
401 SLRHAIQLLSPASVVAKTINGREKMCKADLEEVSGLYLDKSSARLLQEQQ 450
|||||:|||||
384 SLRHAIQLLSPASVVSKTINGREKICKADLEEVSGLYLDKSSARLLQEQQ 433
|||||
451 ERYIT 455
|||||
434 ERYIT 438

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID8 check: 2111 from: 1 to: 456
WPDEF Case 1121 SEQ ID NO: 8 RuVB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuVB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2085	Length:	456
Ratio:	4.760	Gaps:	3
Percent Similarity:	97.717	Percent Identity:	97.489

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID8 x 1121SID10 November 5, 2001 17:14 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDQANGMSMPLAAGFVGQAAAREAA 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLD.ANGMAIALAAGFVG..... 41

51 GLAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGS 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGS 82

101 EVYSSEVKKTEVLMENFRRRAIGLRIVENKEVYEGEVIELSPPEAESTTGG 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
83 EVYSSEVKKTEVLMENFRRRAIGLRIVENKEVYEGEVTLSPEAESTTGG 132

151 YAKSISHVIGLTKTVKGTKQLKLDPSIYDALIKEKVAVGDVIYIEANSGA 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
133 YAKSISHVVISLTKTVKGTKQLKLDSSIYDALIKEKVAVGDVIYIEANSGA 182

201 VKRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
183 VKRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 232

251 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
233 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 282

301 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
283 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 332
```

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Applicant Docket Ref: 1121D

```

351 PVDLLDRLVLIIRTETYGPTEMIQILAIRAQVEEIDIDEESLAYLGEIGQQ 400
    |||||||||||||||||||||||||||||||||||||||
333 PVDLLDRLVLIIRTETYGPTEMIQILAIRAQVEEIDMDEESLAYLGEIGQQ 382
    .
401 TSLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDAKSSARLLQEQ 450
    |||||||:|||||.|||||.|||||||||||||||||
383 TSLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDAKSSARLLQEQ 432
    .
451 QERYIT 456
    |||||
433 QERYIT 438

```